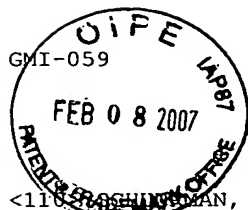


GMI-059



SEQUENCE LISTING

<110> ~~PARSHLOMAN~~, JANINE
 HAVENITH, KARIN
 PARREN, PAUL
 VAN DE WINKEL, JAN
 WILLIAMS, DENISE LEAH
 PETERSEN, JORGEN
 BAADSGAARD, OLE

<120> HUMAN MONOCLONAL ANTIBODIES AGAINST CD25

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<140> 10/714,353

<141> 2003-11-14

<150> 60/426,690

<151> 2002-11-15

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<170> PatentIn Ver. 3.3

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Tyr	
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cct atc aac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg	144
Pro Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	
gga agg atc atc cct atc ctt ggt ata gca gac tac gca cag agg ttc	192
Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asp Tyr Ala Gln Arg Phe	
50 55 60	
cag ggc aga gtc acg att acc gcg gac aaa tcc acg aac aca gcc tac	240
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn Thr Ala Tyr	
65 70 75 80	
atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tat tgt	288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg agg agg gac tgg gga gac tac tgg ggc cag gga acc ctg gtc acc	336
Ala Arg Arg Asp Trp Gly Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	
gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca	381

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 35 40 45
 Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asp Tyr Ala Gln Arg Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
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 100 105 110
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 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
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 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 35 40 45
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Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85          90          95

agc aga ctg gag cct gaa gat ttt gca gtg tat tac tgt cag cag tat 336
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
100        105        110

agt agc tca ccg ctc act ttc ggc gga ggg acc aag gtg gag atc aaa 384
Ser Ser Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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35        40        45

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65          70          75          80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85          90          95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
100        105        110

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 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Tyr
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 35 40 45

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 Gly Arg Ile Ile Pro Ile Leu Asp Ile Ala Asp Tyr Ala Gln Lys Phe
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 Gln Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn Thr Ala Tyr
 65 70 75 80

atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt 288
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga aag gac tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc 336
 Ala Arg Lys Asp Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
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 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
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 35 40 45

Gly Arg Ile Ile Pro Ile Leu Asp Ile Ala Asp Tyr Ala Gln Lys Phe
 50 55 60

Gln Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
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Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala

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120

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 gat atc acc gga gaa aat gtg ttg acg cag tct cca ggc acc ctg tct 96
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 ctg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt 144
 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 35 40 45
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 Gly Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
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 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
 65 70 75 80
 gac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc 288
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 85 90 95
 agc aga ctg gag cct gaa gat ttt gca gtg tat tac tgt cag cag tat 336
 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
 100 105 110
 ggt agt tca ccg atc acc ttc ggc caa ggg aca cga ctg gag att aaa 384
 Gly Ser Ser Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
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 Gly Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
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 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
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 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Tyr
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 Pro Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
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 Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asp Tyr Ala Gln Arg Phe
 50 55 60
 cag ggc aga gtc acg att acc gcg gac aaa ttc acg aac aca gcc tac 240
 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Phe Thr Asn Thr Ala Tyr
 65 70 75 80
 atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tat tgt 288
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg agg agg gac tgg gga gac tac tgg ggc cag gga acc ctg gtc acc 336
 Ala Arg Arg Asp Trp Gly Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
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	85	90	95	
agc aga ctg gag cct gaa gat ttt gca gtg tat tac tgt cag cag tat				336
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr				
	100	105	110	
agt agc tca ccg ctc act ttc ggc gga ggg acc aag gtg gag atc aaa				384
Ser Ser Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys				
	115	120	125	
cga act gtg gct gca cca tct gtc ttc atc ttc ccc g				421
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro				
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 35 40 45
 Val Ser Ser Ser Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 50 55 60
 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
 65 70 75 80
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 85 90 95
 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
 100 105 110
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 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
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tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc agg tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Tyr
          20           25           30

att atc aac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
Ile Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35           40           45

gga agg atc atc cct atc ctt ggt gta gaa aac tac gca cag aag ttc 192
Gly Arg Ile Ile Pro Ile Leu Gly Val Glu Asn Tyr Ala Gln Lys Phe
          50           55           60

cag ggc aga gtc acg att acc gcg gac aaa tcc acg agc aca gcc tac 240
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
          65           70           75           80

atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt 288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85           90           95

gcg aga aag gac tgg ttt gat tac tgg ggc cag gga acc ctg gtc acc 336
Ala Arg Lys Asp Trp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
          100           105           110

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Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
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Ile Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35           40           45

Gly Arg Ile Ile Pro Ile Leu Gly Val Glu Asn Tyr Ala Gln Lys Phe
          50           55           60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
          65           70           75           80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85           90           95

Ala Arg Lys Asp Trp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
          100           105           110

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 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
 20 25 30

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 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 35 40 45

gtt agc agc tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc 192
 Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
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 Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp
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agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc 288
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95

aga ctg gag cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt 336
 Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
 100 105 110

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 Ser Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
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Ser	Ser	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg															
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cccgtcagc tcctggggct cctg 24

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ccctgctcag ctctggggc tgc 23

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<210> 62
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filed for detailed description of preferred embodiments

<220>
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filed for detailed description of preferred embodiments

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filed for detailed description of preferred embodiments

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<220>
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Xaa

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 <212> PRT
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 1 5 10 15

Xaa

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Xaa

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 filed for detailed description of preferred embodiments

<400> 66
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<210> 67
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 <223> Phe, Trp or Tyr

<400> 67
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 1 5 10

<210> 68
 <211> 11
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 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (6)
 <223> Val or Gly

<220>
 <221> MOD_RES
 <222> (9)
 <223> Phe or Tyr

<400> 68
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<210> 69
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 <212> PRT
 <213> Homo sapiens

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<210> 70
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<213> Homo sapiens

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5

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<211> 96

<212> PRT

<213> Homo sapiens

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5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85

90

95

<210> 72

<211> 98

<212> PRT

<213> Homo sapiens

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

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5

10

15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr

20

25

30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe

50

55

60

GMI-059

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
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Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg

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filed for detailed description of preferred embodiments

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filed for detailed description of preferred embodiments

<400> 73
Xaa Tyr Xaa Ile Xaa
1 5

<210> 74
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<222> (5)
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1 5